

File Copy
09/757,049
updated

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	12D06
Mailbox room#:	11E12
Phone:	(703) 308-8365
Results Format:	paper

Serial #:09/757049

Please Search:

Nucleic Acid databases for:

SEQ ID No: 13, 15, 21, 22 and 27

Including:

1. Interference Search Only.

These sequences are primers, 12-15 nucleotides in length, so I didn't think special permission was required. Please let me know if this is otherwise.

Thanks,
Dave.

TFSEARCH Search Result

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Page 1 of 1

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updated

Transcription Factor Binding Site
TFSEARCH Search Result *Search*

** TFSEARCH ver.1.3 ** (c)1995 Yutaka Akiyama (Kyoto Univ.)

This simple routine searches highly correlated sequence fragments versus TFMATRIX transcription factor binding site profile database by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!


Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (9 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

	entry	score
1	TTAACATAA	

Total 0 high-scoring sites found.

** No TFMATRIX entry hit for your sequence. **

-
- [TRANSFAC database document \(Notice to users\)](#)
 - [TFMATRIX: binding site distribution matrix](#)
 - [Parallel Application Tsukuba Laboratory Home Page](#)
 -  [PAPIA system Top Page](#)

TFSEARCH Search Result

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<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (12 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

	entry	score
1	GATTTACCAT AA	

Total 0 high-scoring sites found.

** No TFMATRIX entry hit for your sequence. **

● [TRANSFAC database document \(Notice to users\)](#)

● [TFMATRIX: binding site distribution matrix](#)

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TFSEARCH Search Result

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This simple routine searches highly correlated sequence fragments versus TFMATRIX transcription factor binding site profile database by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (16 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

1 AATAAAATCA AAAATT

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entry	score
<u>M00148</u> SRY	90.9
<u>M00100</u> CdxA	87.2

Total 2 high-scoring sites found.
Max score: 90.9 point, Min score: 87.2 point

● [TRANSFAC database document \(Notice to users\)](#)

● [TFMATRIX: binding site distribution matrix](#)

● [Parallel Application Tsukuba Laboratory Home Page](#)

●



[PAPIA system Top Page](#)

TFSEARCH Search Result

** TFSEARCH ver.1.3 ** (c)1995 Yutaka Akiyama (Kyoto Univ.)

This simple routine searches highly correlated sequence fragments
versus TFMATRIX transcription factor binding site profile database
by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (15 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

1 AAAGGGGAAC ACTTT

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entry		score
<u>M00029</u>	HSF	90.9
<u>M00154</u>	STRE	89.6
<u>M00048</u>	ADR1	89.2
<u>M00083</u>	MZF1	88.7

Total 4 high-scoring sites found.
Max score: 90.9 point, Min score: 88.7 point

-
- [TRANSFAC database document \(Notice to users\)](#)
 - [TFMATRIX: binding site distribution matrix](#)
 - [Parallel Application Tsukuba Laboratory Home Page](#)
 -  [PAPIA system Top Page](#)

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ECDC Back to the ECDC Homepage
On

Promoters

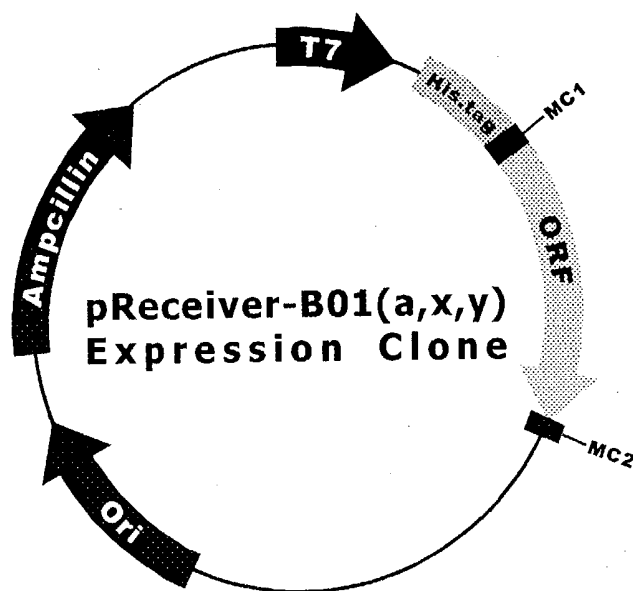
From E. Coli

Genname	ECD AccNr	map position	Sequence source (start-end)	Contig	C
<u>agaY</u>	CO05664	<u>70.69</u>	<u>U18997</u> (63895-64755)	<u>ECD065.00</u>	-
<u>CP05102</u>	CP05102	<u>92.85</u>	<u>U14003</u> (2010-1983)	<u>ECD090.00</u>	-
<u>CP05103</u>	CP05103	<u>92.89</u>	<u>U14003</u> (3979-3952)	<u>ECD090.00</u>	-
<u>CP05104</u>	CP05104	<u>93.16</u>	<u>U14003</u> (16362-16335)	<u>ECD090.00</u>	-
<u>CP05105</u>	CP05105	<u>93.16</u>	<u>U14003</u> (16742-16713)	<u>ECD090.00</u>	-
<u>CP05106</u>	CP05106	<u>93.18</u>	<u>U14003</u> (17659-17631)	<u>ECD090.00</u>	-
<u>CP05107</u>	CP05107	<u>93.19</u>	<u>U14003</u> (17695-17724)	<u>ECD090.00</u>	-
<u>CP05108</u>	CP05108	<u>93.26</u>	<u>U14003</u> (21114-21142)	<u>ECD090.00</u>	-
<u>CP05109</u>	CP05109	<u>93.33</u>	<u>U14003</u> (24224-24196)	<u>ECD090.00</u>	-
<u>CP05110</u>	CP05110	<u>93.40</u>	<u>U14003</u> (27865-27840)	<u>ECD090.00</u>	-
<u>CP05111</u>	CP05111	<u>93.43</u>	<u>U14003</u> (28905-28876)	<u>ECD090.00</u>	-
<u>CP05112</u>	CP05112	<u>93.48</u>	<u>U14003</u> (31418-31390)	<u>ECD090.00</u>	-
<u>CP05113</u>	CP05113	<u>93.59</u>	<u>U14003</u> (36386-36358)	<u>ECD090.00</u>	-
<u>CP05114</u>	CP05114	<u>93.66</u>	<u>U14003</u> (39819-39792)	<u>ECD090.00</u>	-
<u>CP05115</u>	CP05115	<u>93.68</u>	<u>U14003</u> (40912-40885)	<u>ECD090.00</u>	-
<u>CP05116</u>	CP05116	<u>93.72</u>	<u>U14003</u> (42672-42645)	<u>ECD090.00</u>	-
<u>CP05117</u>	CP05117	<u>93.73</u>	<u>U14003</u> (43142-43170)	<u>ECD090.00</u>	-
<u>CP05118</u>	CP05118	<u>93.79</u>	<u>U14003</u> (45667-45640)	<u>ECD090.00</u>	-
<u>CP05119</u>	CP05119	<u>93.90</u>	<u>U14003</u> (51137-51110)	<u>ECD090.00</u>	-
<u>CP05120</u>	CP05120	<u>93.94</u>	<u>U14003</u> (52808-52791)	<u>ECD090.00</u>	-
<u>CP05121</u>	CP05121	<u>94.01</u>	<u>U14003</u> (55951-55924)	<u>ECD090.00</u>	-
<u>CP05122</u>	CP05122	<u>94.05</u>	<u>U14003</u> (57814-57786)	<u>ECD090.00</u>	-
<u>CP05123</u>	CP05123	<u>94.08</u>	<u>U14003</u> (59230-59203)	<u>ECD090.00</u>	-
<u>CP05124</u>	CP05124	<u>94.09</u>	<u>U14003</u> (59507-59536)	<u>ECD090.00</u>	-
<u>CP05125</u>	CP05125	<u>94.12</u>	<u>U14003</u> (61315-61344)	<u>ECD090.00</u>	-
<u>CP05126</u>	CP05126	<u>94.21</u>	<u>U14003</u> (65199-65171)	<u>ECD090.00</u>	-
<u>CP05127</u>	CP05127	<u>94.24</u>	<u>U14003</u> (66565-66537)	<u>ECD090.00</u>	-
<u>CP05128</u>	CP05128	<u>94.31</u>	<u>U14003</u> (69866-69839)	<u>ECD090.00</u>	-
<u>CP05129</u>	CP05129	<u>94.38</u>	<u>U14003</u> (73279-73252)	<u>ECD090.00</u>	-
<u>CP05130</u>	CP05130	<u>94.38</u>	<u>U14003</u> (73410-73438)	<u>ECD090.00</u>	-
<u>CP05131</u>	CP05131	<u>94.41</u>	<u>U14003</u> (74554-74583)	<u>ECD090.00</u>	-
<u>CP05132</u>	CP05132	<u>94.53</u>	<u>U14003</u> (80245-80217)	<u>ECD090.00</u>	-
<u>CP05133</u>	CP05133	<u>94.55</u>	<u>U14003</u> (81288-81260)	<u>ECD090.00</u>	-
<u>CP05134</u>	CP05134	<u>94.58</u>	<u>U14003</u> (82270-82297)	<u>ECD090.00</u>	-
<u>CP05135</u>	CP05135	<u>94.63</u>	<u>U14003</u> (84824-84840)	<u>ECD090.00</u>	-
<u>CP05136</u>	CP05136	<u>94.63</u>	<u>U14003</u> (84955-84927)	<u>ECD090.00</u>	-
<u>CP05137</u>	CP05137	<u>94.76</u>	<u>U14003</u> (91027-91054)	<u>ECD090.00</u>	-
<u>CP05138</u>	CP05138	<u>94.85</u>	<u>U14003</u> (95106-95135)	<u>ECD090.00</u>	-
<u>CP05139</u>	CP05139	<u>94.89</u>	<u>U14003</u> (96837-96866)	<u>ECD090.00</u>	-
<u>CP05140</u>	CP05140	<u>94.97</u>	<u>U14003</u> (100809-100837)	<u>ECD090.00</u>	-
<u>CP05141</u>	CP05141	<u>95.11</u>	<u>U14003</u> (107270-107242)	<u>ECD090.00</u>	-
<u>CP05142</u>	CP05142	<u>95.16</u>	<u>U14003</u> (109285-109257)	<u>ECD090.00</u>	-
<u>CP05143</u>	CP05143	<u>95.18</u>	<u>U14003</u> (110501-110472)	<u>ECD090.00</u>	-
<u>CP05144</u>	CP05144	<u>95.19</u>	<u>U14003</u> (110739-110766)	<u>ECD090.00</u>	-
<u>CP05145</u>	CP05145	<u>95.30</u>	<u>U14003</u> (115823-115851)	<u>ECD090.00</u>	-
<u>CP05146</u>	CP05146	<u>95.35</u>	<u>U14003</u> (118355-118327)	<u>ECD090.00</u>	-

EP03730	CP03730	87.77	L19201	(37133-37161)	ECD085.00	-
EP03731	CP03731	87.85	L19201	(40642-40670)	ECD085.00	-
EP03732	CP03732	87.86	L19201	(41165-41194)	ECD085.00	-
EP03733	CP03733	88.00	L19201	(47579-47552)	ECD085.00	-
EP03734	CP03734	88.00	L19201	(47674-47701)	ECD085.00	-
EP03735	CP03735	88.02	L19201	(48522-48551)	ECD085.00	-
EP03736	CP03736	88.14	L19201	(54487-54461)	ECD085.00	-
EP03737	CP03737	88.14	L19201	(54505-54477)	ECD085.00	-
EP03738	CP03738	88.18	L19201	(56031-56003)	ECD085.00	-
EP03739	CP03739	88.24	L19201	(59140-59112)	ECD085.00	-
EP03740	CP03740	88.25	L19201	(59215-59186)	ECD085.00	-
EP03741	CP03741	88.25	L19201	(59347-59376)	ECD085.00	-
EP03742	CP03742	88.31	L19201	(62227-62198)	ECD085.00	-
EP03743	CP03743	88.31	L19201	(62358-62385)	ECD085.00	-
EP03744	CP03744	88.33	L19201	(63274-63302)	ECD085.00	-
EP03745	CP03745	88.36	L19201	(64316-64347)	ECD085.00	-
EP03746	CP03746	88.36	L19201	(64317-64345)	ECD085.00	-
EP03747	CP03747	88.42	L19201	(67337-67308)	ECD085.00	-
EP03748	CP03748	88.42	L19201	(67390-67419)	ECD085.00	-
EP03749	CP03749	88.44	L19201	(68037-68053)	ECD085.00	-
EP03750	CP03750	88.44	L19201	(68048-68075)	ECD085.00	-
EP03751	CP03751	88.46	L19201	(69069-69098)	ECD085.00	-
EP03752	CP03752	88.46	L19201	(69089-69105)	ECD085.00	-
EP03753	CP03753	88.49	L19201	(70382-70409)	ECD085.00	-
EP03754	CP03754	88.51	L19201	(71505-71532)	ECD085.00	-
EP03755	CP03755	88.55	L19201	(73238-73210)	ECD085.00	-
EP03756	CP03756	88.56	L19201	(73865-73893)	ECD085.00	-
EP03757	CP03757	88.56	L19201	(73906-73878)	ECD085.00	-
EP03758	CP03758	88.57	L19201	(74446-74475)	ECD085.00	-
EP03759	CP03759	88.69	L19201	(79829-79801)	ECD085.00	-
EP03760	CP03760	88.69	L19201	(80024-80052)	ECD085.00	-
EP03761	CP03761	88.71	L19201	(81025-80996)	ECD085.00	-
EP03762	CP03762	88.74	L19201	(82022-81993)	ECD085.00	-
EP03763	CP03763	88.78	L19201	(84019-83990)	ECD085.00	-
EP03764	CP03764	88.80	L19201	(85038-85010)	ECD085.00	-
EP03765	CP03765	88.82	L19201	(86148-86119)	ECD085.00	-
EP03766	CP03766	88.88	L19201	(88577-88550)	ECD085.00	-
EP03767	CP03767	88.88	L19201	(88557-88586)	ECD085.00	-
EP03768	CP03768	88.88	L19201	(88586-88557)	ECD085.00	-
EP03769	CP03769	88.90	L19201	(89533-89505)	ECD085.00	-
EP03770	CP03770	88.91	L19201	(90226-90197)	ECD085.00	-
EP03771	CP03771	88.91	L19201	(90233-90261)	ECD085.00	-
EP03772	CP03772	89.00	L19201	(94148-94176)	ECD085.00	-
EP03773	CP03773	89.02	L19201	(95410-95437)	ECD085.00	-
EP03776	CP03776	0.64	X70017	(118-144)	ECD000.00	-
EP03777	CP03777	0.64	X70017	(186-216)	ECD000.00	-
EP03779	CP03779	60.70	L07596	(682-708)	ECD060.00	-
EP03780	CP03780	27.98	M60918	(548-576)	ECD025.00	-
EP03781	CP03781	27.99	M60918	(792-821)	ECD025.00	-
EP04713	CP04713	17.51	M29632	(35-49)	ECD015.00	-
EP04714	CP04714	78.57	X80057	(655-683)	ECD075.00	-
EP04720	CP04720	93.66	X79886	(128-146)	ECD090.00	-
EP04725	CP04725	99.59	L27665	(32-72)	ECD095.00	-
EP04740	CP04740	39.10	J01615	(91-121)	ECD039.10	-
EP04741	CP04741	60.17	X65104	(136-149)	ECD060.00	-
lacP	CP00848	7.87	J01636	(1201-1275)	ECD005.00	-
lacP _{uv5}	CP02815	7.87	K01793	(1-67)	ECD005.00	-
p-bqIX	CP04882	47.84	U15049	(34-63)	ECD045.00	-
p-clS	CP04897	28.16	U15986	(77-104)	ECD025.00	-
p-cytRP	CP03782	88.83	X68638	(1-111)	ECD085.00	-

<u>p-dsrA</u>	CP05856	<u>43.60</u>	<u>U17136</u>	(865-893)	<u>ECD040.00</u>	-
<u>p-fadL</u>	CP03703	<u>52.99</u>	<u>X70445</u>	(1-166)	<u>ECD050.00</u>	-
<u>p-fyuA</u>	CP04888	-	<u>Z38064</u>	(74-101)	-	-
<u>p-hho</u>	CP04893	<u>72.80</u>	<u>U15661</u>	(454-482)	<u>ECD070.00</u>	-
<u>p-nfs</u>	CP04879	<u>13.03</u>	<u>D25414</u>	(138-166)	<u>ECD010.00</u>	-
<u>p-torR</u>	CP04875	<u>22.78</u>	<u>X78195</u>	(2184-2156)	<u>ECD020.00</u>	-
<u>pEmrR</u>	CP05908	<u>60.53</u>	<u>U19993</u>	(255-283)	<u>ECD060.00</u>	-
<u>pqi5B</u>	CG06186	<u>21.82</u>	<u>X81561</u>	(2108-2382)	<u>ECD020.00</u>	-

OmicsLink™ Clone (T7 Promoter)



pReceiver-B01a

T7 Promoter His.tag Xmn I ORF Xho I Not I rb
 TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATATACATATG TCG
 TAC TAC CAT CAC CAT CAC CAT CAT CAC GAA GGA GTT CGA ACC ATG TAGCTCGAGTGC GGCCGCA
 Nsp V

pReceiver-B01x

T7 Promoter His.tag Xmn I Kpn I ORF Xho I Not I rb
 TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATATACATATG TCG
 TAC TAC CAT CAC CAT CAC CAT CAT TCG AAG GAA TTC GGT ACC ATG TAGCTCGAGTGC GGCCGCA
 EcoR I

pReceiver-B01y

T7 Promoter His.tag ORF Xho I Not I rb
 TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATATACATATG TCG
 TAC TAC CAT CAC CAT CAC CAT CAT CAC GAA GGA ACC ACC ATG TAGCTCGAGTGC GGCCGCA

Regulatory elements and transcriptional factors

For Yeast

Get factor & element list	Get consensus list	Get matrix list
Get distribution of mapped sites		Get summary of distribution
Get correlation between factors		
Search	none	

Main

ABF1 TCRNNNNNNACG
 ACE2 GCTGGT
 ADR1 TCTCC
 AP-1 TTANTAA
 ATF ACGTCA
 BAS2 TAATRA
 BAS2 TAANTAA
 CPF1 TCACGTG
 CuRE GAGCAA
 CSRE YCGGAYRRWGG
 SCB CNCGAAA
 GC/FAR CCCGGG
 GC/FAR GGGCCC
 GAL4 CGGNNNNNNNNNNCCG
 GCN4 TGANTN
 GCR1 CWTCC
 HAP1 CGGNNNTANCGG
 HSTF GAANNNTCC
 HSTF GAANNNTCC
 HSTF TTCNNGAA
 HSTF TTCNNGAA
 LEU3 CCGNNNNCCG or GGCNNNNGCC
 MCB WCGCGW
 MCM1 CCNNNWWRRG
 MATApha2 CRTGTWWWW
 MIG1 CCCCRNNWWWW
 MSE CRCAA
 NBF ATGYGRAWW
 PHO4 CACGTK
 PDR3 TCCGYGGA
 PPR1 TTCGGNNNNNNCCGAA
 PUT3 CGGNNNNNNNNNNCCG
 REB1 YYACCCG
 ROX1 YYNATTGTTY
 RAP1 RMACCCA
 RME1 GAACCTCAA
 repressor_of_CAR1 AGCCGCSA
 SWI5 KGCTGR
 STE12 TGAAACA
 TBP TATAWAW
 T4C TTTTCTYCG
 TEA1 CGGNNNNNNNNNNCCG
 UASPHR CTTCTT
 URSPHR GTSAAAGTAWG

UASRAD	WTTTCCCGS
UASINO	ATGTGAAWW
SFF	GTMAACAA
ECB	GGAAAAD
STRE	AGGGG
ORC	WTTTATRTTTW

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updated

CMV promoter sequence

TAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAAT
GGCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACG
CCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAA
GTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATG
CGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCCAT
GACGTCAATGGGAGTTTGTGTTTGGCACCAAATCAACGGGACTTTCCTCAAAATGTCGTAACAACTCCGCCCCA
TTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAG

pBV-Luc Vector Map**pBV-Luc Vector Sequence**